The Yeast Vacuolar Membrane Proteome

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Table S1 Processing of biological replicates

Labeling combinations and grouping of biological samples. For the experiment, four biological replicates were used. Two biological samples were labeled with four different iTRAQ reagents (to label peptides from proteins in crude and pure vacuolar membranes) and combined labeled peptides were fractionated using SCX.

Biological replicate 1 Quantification **114/116**		Biological replicate 2 Quantification **115/117**		Biological replicate 3 Quantification **116/114**		Biological replicate 4 Quantification **117/115**	
Pure membranes	Crude membranes	Pure membranes	Crude membranes	Pure membranes	Crude membranes	Pure membranes	Crude membranes
114	116	115	117	116	114	117	115
SCX 1				**SCX 2**			

Table S2 Double-boundary iGA results

The double-boundary iGA yielded significant clustering for different groups of proteins for which the probability of change (PC-) values are shown. The significance of clustering was tested using a multiple-testing procedure; corrected p-values below 0.001 indicate high significance, corrected p-values above 0.005 were regarded as insignificant.

Group	Range	PC-value	Number of group members (Total) Above-**within**-below Boundaries	**Corrected p-value**
SIGNIFICANT CLUSTERS				
Vacuole	1–148	3.4×10^{-37}	(77) 0-**69**-8	**<0.001**
Endosome	88-214	1.9×10^{-9}	(13) 0-**13**-0	**<0.001**
Mitochondrion	326-570	1.9×10^{-12}	(127) 37-**89**-1	**<0.001**
INSIGNIFICANT CLUSTERS				
Cytosol	98-505	1.5×10^{-5}	(127) 8-**109**-10	0.013
ER	211-518	9.7×10^{-6}	(74) 14-**57**-3	0.008
Golgi	55–256	6×10^{-4}	(33) 1-**21**-11	0.251
Nucleus	279-381	1.5×10^{-5}	(38) 7-**8**-13	0.017
Plasma membrane	7-310	4×10^{-4}	(39) 0-**31**-8	0.249